



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/766,752  
Source: 1 FWO  
Date Processed by STIC: 2/9/04

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221**

**Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/766,752

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                   (xi)  SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                   This sequence is intentionally skipped  
  
                                   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                   <210> sequence id number  
                                   <400> sequence id number  
                                   000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                   Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                   In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11 ✓ Use of <220>     Sequence(s) 2-6 missing the <220> "Feature" and associated numeric identifiers and responses.  
                                   Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/766,752

DATE: 02/09/2004

TIME: 10:32:41

Input Set : A:\30331008008.txt

Output Set: N:\CRF4\02062004\J766752.raw

4 <110> APPLICANT: Carney, Darrell H.  
6 <120> TITLE OF INVENTION: Use of Thrombin-Derived Peptides for the Therapy  
7 of Chronic Dermal Ulcers  
9 <130> FILE REFERENCE: 3033.1008-008

C--&gt; 11 &lt;140&gt; CURRENT APPLICATION NUMBER: US/10/766,752

C--&gt; 12 &lt;141&gt; CURRENT FILING DATE: 2004-01-27

14 &lt;150&gt; PRIOR APPLICATION NUMBER: PCT/US02/01151

15 &lt;151&gt; PRIOR FILING DATE: 2002-01-16

17 &lt;150&gt; PRIOR APPLICATION NUMBER: US 60/308,198

18 &lt;151&gt; PRIOR FILING DATE: 2001-07-27

20 &lt;160&gt; NUMBER OF SEQ ID NOS: 6

22 &lt;170&gt; SOFTWARE: FastSEQ for Windows Version 4.0

24 &lt;210&gt; SEQ ID NO: 1

25 &lt;211&gt; LENGTH: 23

26 &lt;212&gt; TYPE: PRT

27 &lt;213&gt; ORGANISM: Artificial Sequence

29 &lt;220&gt; FEATURE:

30 &lt;223&gt; OTHER INFORMATION: fragment of human thrombin

32 &lt;400&gt; SEQUENCE: 1

33 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Glu Gly

34 1 5 10 15

35 Asp Ser Gly Gly Pro Phe Val

36 20

39 &lt;210&gt; SEQ ID NO: 2

40 &lt;211&gt; LENGTH: 23

41 &lt;212&gt; TYPE: PRT

42 &lt;213&gt; ORGANISM: Artificial Sequence

44 &lt;220&gt; FEATURE:

45 &lt;223&gt; OTHER INFORMATION: Alanine at position 1 is optionally N-acylated.

47 &lt;223&gt; OTHER INFORMATION: Valine at position 23 is optionally C-amidated.

W--&gt; 49 &lt;221&gt; NAME/KEY: VARIANT

W--&gt; 50 &lt;222&gt; LOCATION: 15

W--&gt; 51 &lt;223&gt; Xaa = Glu or Gln

W--&gt; 53 &lt;221&gt; NAME/KEY: VARIANT

W--&gt; 54 &lt;222&gt; LOCATION: (22)...(22)

W--&gt; 55 &lt;223&gt; Xaa = Phe, Met, Leu, His or Val

W--&gt; 58 &lt;400&gt; 2

W--&gt; 59 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Xaa Gly

60 1 5 10 15

61 Asp Ser Gly Gly Pro Xaa Val

62 20

65 &lt;210&gt; SEQ ID NO: 3

66 &lt;211&gt; LENGTH: 33

Does Not Comply  
Corrected Diskette Needed

pp 1-3

needs explanation in <2207-2223>  
section.

(see  
item 11  
on Error  
Summary  
Sheet)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/766,752

DATE: 02/09/2004

TIME: 10:32:41

Input Set : A:\30331008008.txt

Output Set: N:\CRF4\02062004\J766752.raw

67 <212> TYPE: PRT

68 <213> ORGANISM: Artificial Sequence

70 <220> FEATURE:

71 <223> OTHER INFORMATION: Asparatic acid at position 1 is optionally

72 N-acylated.

74 <223> OTHER INFORMATION: Phenylalanine at position 33 is optionally

75 C-amidated.

*see item 11 on Error Summary sheet*

W--> 77 <400> 3

78 Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly

79 1 5 10 15

80 Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Phe Val Met Lys Ser Pro

81 20 25 30

82 Phe

86 <210> SEQ ID NO: 4

87 <211> LENGTH: 33

88 <212> TYPE: PRT

89 <213> ORGANISM: Artificial Sequence

*same error*

91 <220> FEATURE:

92 <223> OTHER INFORMATION: Asparatic acid at position 1 is optionally

93 N-acylated.

95 <223> OTHER INFORMATION: Phenylalanine at position 33 is optionally

96 C-amidated.

W--> 98 <221> NAME/KEY: VARIANT

W--> 99 <222> LOCATION: (20)...(20)

W--> 100 <223> Xaa = Glu or Gln

W--> 102 <221> NAME/KEY: VARIANT

W--> 103 <222> LOCATION: (27)...(27)

W--> 104 <223> Xaa = Phe, Met, Leu, His or val

W--> 106 <400> 4

107 Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly

108 1 5 10 15

W--> 109 Asp Ala Cys Xaa Gly Asp Ser Gly Gly Pro Xaa Val Met Lys Ser Pro

110 20 25 30

111 Phe

115 <210> SEQ ID NO: 5

116 <211> LENGTH: 23

117 <212> TYPE: PRT

118 <213> ORGANISM: Artificial Sequence

*same*

120 <220> FEATURE:

121 <223> OTHER INFORMATION: Alanine at position 1 is optionally N-acylated.

123 <223> OTHER INFORMATION: Valine at position 23 is optionally C-amidated.

W--> 128 <400> 5

129 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Glu Gly

130 1 5 10 15

131 Asp Ser Gly Gly Pro Phe Val

132 20

135 <210> SEQ ID NO: 6

136 <211> LENGTH: 23

137 <212> TYPE: PRT

## RAW SEQUENCE LISTING

DATE: 02/09/2004

PATENT APPLICATION: US/10/766,752

TIME: 10:32:41

Input Set : A:\30331008008.txt

Output Set: N:\CRF4\02062004\J766752.raw

138 &lt;213&gt; ORGANISM: Artificial Sequence

*same*

140 &lt;220&gt; FEATURE:

141 <223> OTHER INFORMATION: Valine at position 23 is amidated with -NH<sub>2</sub>.

143 &lt;400&gt; SEQUENCE: 6

144 Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg Gly Asp Ala Cys Glu Gly

145 1 5 10 15

146 Asp Ser Gly Gly Pro Phe Val

147 20

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/766,752

DATE: 02/09/2004  
TIME: 10:32:42

Input Set : A:\30331008008.txt  
Output Set: N:\CRF4\02062004\J766752.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 15,22

Seq#:4; Xaa Pos. 20,27

**VERIFICATION SUMMARY**

DATE: 02/09/2004

PATENT APPLICATION: US/10/766,752

TIME: 10:32:42

Input Set : A:\30331008008.txt

Output Set: N:\CRF4\02062004\J766752.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:49 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:50 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:51 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:53 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:54 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:55 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:58 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
M:341 Repeated in SeqNo=2  
L:77 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:98 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:99 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:100 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:102 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:103 M:281 W: Numeric Fields not Ordered, <222> Sort in ascending order!  
L:104 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:106 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16  
L:128 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5